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TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/634,252A

DATE: 06/01/2001

TIME: 14:29:35

Input Set : A:\SVP3137.txt.txt

Output Set: C:\CRF3\06012001\I634252A.raw

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3 <110> APPLICANT: Cerretti, Douglas P.
5 <120> TITLE OF INVENTION: SVP3-13 AND SVP3-17 DNA AND POLYPEPTIDES
7 <130> FILE REFERENCE: 03260.0051-00304
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/634,252A
C--> 10 <141> CURRENT FILING DATE: 2000-08-07
12 <150> PRIOR APPLICATION NUMBER: 60/074,310
13 <151> PRIOR FILING DATE: 1998-02-11
15 <160> NUMBER OF SEQ ID NOS: 10
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 58
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <400> SEQUENCE: 1
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29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
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39 atcaaccaag actcgaaag cccttatcac gttcttgaca caaaggcaag acaccagcaa 420
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61 cgggatgctg tgaacgagtg tgatattact gaattattgta ctggagactc tggtcagtg 1740
62 ccaccaaadc ttcataagca agacggatat gcatgcaatc aaaatcaggg ccgctgctac 1800
63 aatggcgagt gcaagaccag agacaaccag tgtcagtaca tctggggaac aaaggctgca 1860
64 gggctctgaca agttctgcta tgaaaagctg aatacagaag gcaactgagaa gggaaactgc 1920
65 gggaaggatg gagaccgggt gattcagtg agcaaacatg atgtgttctg tggattctta 1980
66 ctctgtacca atcttactcg agctccacgt attgggtcaac ttcagggtga gatcattcca 2040
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68 gatgatacgg atgtgggcta tgtagaagat ggaacgccat gtggcccgtc tatgatgtgt 2160
69 ttagatcgga agtgcctaca aattcaagcc ctaaatatga gcagctgtcc actcgattcc 2220
70 aagggtaaaag tctgttcggg ccattgggtg tgtagtaatg aagccacctg catttgatgt 2280
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72 aaggatgaag gacccaaggg tcctagtgcc accaatctca taataggctc catcgctggt 2400
73 gccatcctgg tagcagctat tgccttggg ggcacaggct ggggatitaa aaatgtcaag 2460
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76 <210> SEQ ID NO: 3

77 <211> LENGTH: 20

78 <212> TYPE: PRT

79 <213> ORGANISM: Homo sapiens

81 <400> SEQUENCE: 3

82 Leu Leu Asp Pro Pro Glu Cys Gly Asn Gly Phe Ile Glu Thr Gly Glu

83 1 5 10 15

85 Glu Cys Asp Cys

86 20

89 <210> SEQ ID NO: 4

90 <211> LENGTH: 832

91 <212> TYPE: PRT

92 <213> ORGANISM: Homo sapiens

94 <400> SEQUENCE: 4

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96 1 5 10 15

98 Ser Leu Ala Gly Ala Ser Cys Gly Pro Gln Arg Gly Pro Ala Gly Ser

99 20 25 30

101 Val Pro Ala Ser Ala Pro Ala Arg Thr Pro Pro Cys Arg Leu Leu Leu

102 35 40 45

104 Val Leu Leu Leu Leu Pro Pro Leu Ala Ala Ser Ser Arg Pro Arg Ala

105 50 55 60

107 Trp Gly Ala Ala Ala Pro Ser Ala Pro His Trp Asn Glu Thr Ala Glu

108 65 70 75 80

110 Lys Asn Leu Gly Val Leu Ala Asp Glu Asp Asn Thr Leu Gln Gln Asn

111 85 90 95

113 Ser Ser Ser Asn Ile Ser Tyr Ser Asn Ala Met Gln Lys Glu Ile Thr

114 100 105 110

116 Leu Pro Ser Arg Leu Ile Tyr Tyr Ile Asn Gln Asp Ser Glu Ser Pro

117 115 120 125

119 Tyr His Val Leu Asp Thr Lys Ala Arg His Gln Gln Lys His Asn Lys

120 130 135 140

122 Ala Val His Leu Ala Gln Ala Ser Phe Gln Ile Glu Ala Phe Gly Ser

123 145 150 155 160

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125 Lys Phe Ile Leu Asp Leu Ile Leu Asn Asn Gly Leu Leu Ser Ser Asp
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128 Tyr Val Glu Ile His Tyr Glu Asn Gly Lys Pro Gln Tyr Ser Lys Gly
129          180          185          190
131 Gly Glu His Cys Tyr Tyr His Gly Ser Ile Arg Gly Val Lys Asp Ser
132          195          200          205
134 Lys Val Ala Leu Ser Thr Cys Asn Gly Leu His Gly Met Phe Glu Asp
135          210          215          220
137 Asp Thr Phe Val Tyr Met Ile Glu Pro Leu Glu Leu Val His Asp Glu
138 225          230          235          240
140 Lys Ser Thr Gly Arg Pro His Ile Ile Gln Lys Thr Leu Ala Gly Gln
141          245          250          255
143 Tyr Ser Lys Gln Met Lys Asn Leu Thr Met Glu Arg Gly Asp Gln Trp
144          260          265          270
146 Pro Phe Leu Ser Glu Leu Gln Trp Leu Lys Arg Arg Lys Arg Ala Val
147          275          280          285
149 Asn Pro Ser Arg Gly Ile Phe Glu Glu Met Lys Tyr Leu Glu Leu Met
150          290          295          300
152 Ile Val Asn Asp His Lys Thr Tyr Lys Lys His Arg Ser Ser His Ala
153 305          310          315          320
155 His Thr Asn Asn Phe Ala Lys Ser Val Val Asn Leu Val Asp Ser Ile
156          325          330          335
158 Tyr Lys Glu Gln Leu Asn Thr Arg Val Val Leu Val Ala Val Glu Thr
159          340          345          350
161 Trp Thr Glu Lys Asp Gln Ile Asp Ile Thr Thr Asn Pro Val Gln Met
162          355          360          365
164 Leu His Glu Phe Ser Lys Tyr Arg Gln Arg Ile Lys Gln His Ala Asp
165          370          375          380
167 Ala Val His Leu Ile Ser Arg Val Thr Phe His Tyr Lys Arg Ser Ser
168 385          390          395          400
170 Leu Ser Tyr Phe Gly Gly Val Cys Ser Arg Thr Arg Gly Val Gly Val
171          405          410          415
173 Asn Glu Tyr Gly Leu Pro Met Ala Val Ala Gln Val Leu Ser Gln Ser
174          420          425          430
176 Leu Ala Gln Asn Leu Gly Ile Gln Trp Glu Pro Ser Ser Arg Lys Pro
177          435          440          445
179 Lys Cys Asp Cys Thr Glu Ser Trp Gly Gly Cys Ile Met Glu Glu Thr
180          450          455          460
182 Gly Val Ser His Ser Arg Lys Phe Ser Lys Cys Ser Ile Leu Glu Tyr
183 465          470          475          480
185 Arg Asp Phe Leu Gln Arg Gly Gly Gly Ala Cys Leu Phe Asn Arg Pro
186          485          490          495
188 Thr Lys Leu Phe Glu Pro Thr Glu Cys Gly Asn Gly Tyr Val Glu Ala
189          500          505          510
191 Gly Glu Glu Cys Asp Cys Gly Phe His Val Glu Cys Tyr Gly Leu Cys
192          515          520          525
194 Cys Lys Lys Cys Ser Leu Ser Asn Gly Ala His Cys Ser Asp Gly Pro
195          530          535          540
197 Cys Cys Asn Asn Thr Ser Cys Leu Phe Gln Pro Arg Gly Tyr Glu Cys

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198 545          550          555          560
200 Arg Asp Ala Val Asn Glu Cys Asp Ile Thr Glu Tyr Cys Thr Gly Asp
201          565          570          575
203 Ser Gly Gln Cys Pro Pro Asn Leu His Lys Gln Asp Gly Tyr Ala Cys
204          580          585          590
206 Asn Gln Asn Gln Gly Arg Cys Tyr Asn Gly Glu Cys Lys Thr Arg Asp
207          595          600          605
209 Asn Gln Cys Gln Tyr Ile Trp Gly Thr Lys Ala Ala Gly Ser Asp Lys
210          610          615          620
212 Phe Cys Tyr Glu Lys Leu Asn Thr Glu Gly Thr Glu Lys Gly Asn Cys
213 625          630          635          640
215 Gly Lys Asp Gly Asp Arg Trp Ile Gln Cys Ser Lys His Asp Val Phe
216          645          650          655
218 Cys Gly Phe Leu Leu Cys Thr Asn Leu Thr Arg Ala Pro Arg Ile Gly
219          660          665          670
221 Gln Leu Gln Gly Glu Ile Ile Pro Thr Ser Phe Tyr His Gln Gly Arg
222          675          680          685
224 Val Ile Asp Cys Ser Gly Ala His Val Val Leu Asp Asp Asp Thr Asp
225          690          695          700
227 Val Gly Tyr Val Glu Asp Gly Thr Pro Cys Gly Pro Ser Met Met Cys
228 705          710          715          720
230 Leu Asp Arg Lys Cys Leu Gln Ile Gln Ala Leu Asn Met Ser Ser Cys
231          725          730          735
233 Pro Leu Asp Ser Lys Gly Lys Val Cys Ser Gly His Gly Val Cys Ser
234          740          745          750
236 Asn Glu Ala Thr Cys Ile Cys Asp Phe Thr Trp Ala Gly Thr Asp Cys
237          755          760          765
239 Ser Ile Arg Asp Pro Val Arg Asn Leu His Pro Pro Lys Asp Glu Gly
240          770          775          780
242 Pro Lys Gly Pro Ser Ala Thr Asn Leu Ile Ile Gly Ser Ile Ala Gly
243 785          790          795          800
245 Ala Ile Leu Val Ala Ala Ile Val Leu Gly Gly Thr Gly Trp Gly Phe
246          805          810          815
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255 <210> SEQ ID NO: 5

256 <211> LENGTH: 2604

257 <212> TYPE: DNA

258 <213> ORGANISM: Homo sapiens

260 <400> SEQUENCE: 5

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263 ggcggcagtg tgactcatgt tgaccaagca agcttcagg ttgatgcctt tggaacgtca 180
264 ttcattctcg atgtcgtgct aaatcatgat ttgctgtcct ctgaatacat agagagacac 240
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266 catatccgag gaaaccctga ctcatctgtt gcattgtcaa catgccacgg acttcatggg 360
267 atgttctatg acgggaacca cacatatctc attgagccag aagaaaatga cactactcaa 420
268 gaggatttcc attttcattc agtttacaaa tccagactgt ttgaattttc cttggatgat 480
269 cttccatctg aatttcagca agtaaacatt actccatcaa aatttatattt gaagccaaga 540

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272 gtacatacca atacctatgc gaaatctgtg gtgaacatgg cagattttaat atataaagac 720
273 caacttaaga ccaggatagt attggttgct atggaaacct gggcgactga caacaagttt 780
274 gccatatctg aaaatccatt gatcacctta cgtgagttta tgaaatacag gagggatttt 840
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302 actttatctc ctgccaagtc tccttcttca tcaactgggt ctattgcctc cagcagaaaa 2520
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304 aggctatggg agacatccat ttaa 2604

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306 <210> SEQ ID NO: 6

307 <211> LENGTH: 867

308 <212> TYPE: PRT

309 <213> ORGANISM: Homo sapiens

311 <400> SEQUENCE: 6

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316 20 25 30
318 Thr Arg Val Arg Gly Asp Leu Gly Gly Arg Gln Leu Thr His Val Asp
319 35 40 45
321 Gln Ala Ser Phe Gln Val Asp Ala Phe Gly Thr Ser Phe Ile Leu Asp
322 50 55 60
324 Val Val Leu Asn His Asp Leu Leu Ser Ser Glu Tyr Ile Glu Arg His

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date